



## SEQUENCE LISTING

<110> PEPICELLI, CARMEN V.  
LEWIS, PAULA M.  
MCMAHON, ANDREW P.

<120> REGULATION OF LUNG TISSUE BY HEDGEHOG-LIKE POLYPEPTIDES,  
AND FORMULATIONS AND USES RELATED THERETO

<130> HUV-032.01

<140> 09/394,020

<141> 1999-09-10

<150> 60/099,952

<151> 1998-09-11

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<170> PatentIn Ver. 2.1

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Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg	
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Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
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Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
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Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	
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Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser	
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Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	
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Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	
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Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	
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Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val	
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Phe	Thr	Asp	Arg	Asp	Ser	Thr	Thr	Arg	Arg	Val	Phe	Tyr	Val	Ile	Glu	
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Thr	Gln	Glu	Pro	Val	Glu	Lys	Ile	Thr	Leu	Thr	Ala	Ala	His	Leu	Leu	
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Phe	Val	Leu	Asp	Asn	Ser	Thr	Glu	Asp	Leu	His	Thr	Met	Thr	Ala	Ala	
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Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp	
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Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu	
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Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val	
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Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu	
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Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser	
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Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn	
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Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	
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ctg gta tgc tcg gga ctg gcg tgc gga ccg ggc agg ggg ttc ggg aag	96
Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys	
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Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	
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Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	
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Lys	Ile	Ser	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
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Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	
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Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	Ser	
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Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	
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Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	
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Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	
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Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	Asp	Arg	Val	
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Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu	
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Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser	
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Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu	
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Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu	
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Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr	
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Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly	
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Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu	
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Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His	
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Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp	
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Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr	
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Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile	
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His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp	
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Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser	
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Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu Leu Leu																
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Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg Val Val																
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Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys																
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Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg																
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Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr																
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Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly																
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Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu																
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Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr																
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Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr																
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gag ggc cgc gcg gtg gac atc acc aca tca gac cgc gac cgc aat aag																536
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys																
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tat gga ctg ctg gcg cgc ttg gca gtg gag gcc ggc ttt gac tgg gtg																584
Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val																
	165					170						175				

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Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	Gln	Val	
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Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	Pro	Gly	
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Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe	Ser	Asp	
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Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala	Phe	Gln	
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Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	Pro	Ala	
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cac	ctg	ctc	ttt	acg	gct	gac	aat	cac	acg	gag	ccg	gca	gcc	cgc	ttc	920
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Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	Leu	Val	
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Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	Asp	His	
	340					345					350					
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His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His	Ser	Leu	
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Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr	Pro	Gln	
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ctg	ctc	tac	cgc	ctg	ggg	cgt	ctc	ctg	cta	gaa	gag	ggc	agc	ttc	cac	1256
Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser	Phe	His	
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Pro Leu Gly Met Ser Gly Ala Gly Ser  
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Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg																	
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Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe																	
35 40 45																	
gtg ccc ggc gtg cca gag cgg acc ctg ggc gcc agt ggg cca gcg gag	192																
Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu																	
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Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn																	
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Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp																	
85 90 95																	
cgc ctg atg acc gag cgt tgc aag gag agg gtg aac gct ttg gcc att	336																
Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile																	
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gcc gtg atg aac atg tgg ccc gga gtg cgc cta cga gtg act gag ggc	384																
Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly																	
115 120 125																	



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Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
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Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
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Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
165 170 175	
gag tcc cgc aac cac gtc cac gtg tgc gtc aaa gct gat aac tca ctg	576
Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	
180 185 190	
gcg gtc cgg gcg ggc ggc tgc ttt ccg gga aat gca act gtg cgc ctg	624
Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu	
195 200 205	
tgg agc ggc gag cgg aaa ggg ctg cgg gaa ctg cac cgc gga gac tgg	672
Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp	
210 215 220	
gtt ttg gcg gcc gat gcg tca ggc cgg gtg gtg ccc acg ccg gtg ctg	720
Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu	
225 230 235 240	
ctc ttc ctg gac cgg gac ttg cag cgc cgg gct tca ttt gtg gct gtg	768
Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val	
245 250 255	
gag acc gag tgg cct cca cgc aaa ctg ttg ctc acg ccc tgg cac ctg	816
Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu	
260 265 270	
gtg ttt gcc gct cga ggg ccg gcg ccc gcg cca ggc gac ttt gca ccg	864
Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro	
275 280 285	
gtg ttc gcg cgc cgg cta cgc gct ggg gac tgc gtg ctg gcg ccc ggc	912
Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly	
290 295 300	
ggg gat gcg ctt cgg cca gcg cgc gtg gcc cgt gtg gcg cgg gag gaa	960
Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu	
305 310 315 320	
gcc gtg ggc gtg ttc gcg ccg ctc acc gcg cac ggg acg ctg ctg gtg	1008
Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val	
325 330 335	
aac gat gtc ctg gcc tct tgc tac gcg gtt ctg gag agt cac cag tgg	1056
Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp	
340 345 350	

gcg cac cgc gct ttt gcc ccc ttg aga ctg ctg cac gcg cta ggg gcg 1104  
Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala  
355 360 365

ctg ctc ccc ggc ggg gcc gtc cag ccg act ggc atg cat tgg tac tct 1152  
Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser  
370 375 380

cgg ctc ctc tac cgc tta gcg gag gag cta ctg ggc tg 1190  
Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly  
385 390 395

<210> 9

<211> 1251

<212> DNA

<213> Brachydanio rerio

<220>

<221> CDS

<222> (1) .. (1248)

<400> 9

atg gac gta agg ctg cat ctg aag caa ttt gct tta ctg tgt ttt atc 48  
Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile  
1 5 10 15

agc ttg ctt ctg acg cct tgt gga tta gcc tgt ggt cct ggt aga ggt 96  
Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly  
20 25 30

tat gga aaa cga aga cac cca aag aaa tta acc ccg ttg gct tac aag 144  
Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys  
35 40 45

caa ttc atc ccc aac gtt gct gag aaa acg ctt gga gcc agc ggc aaa 192  
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys  
50 55 60

tac gaa ggc aaa atc aca agg aat tca gag aga ttt aaa gag ctg att 240  
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile  
65 70 75 80

ccg aat tat aat ccc gat atc atc ttt aag gac gag gaa aac aca aac 288  
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn  
85 90 95

gct gac agg ctg atg acc aag cgc tgt aag gac aag tta aat tcg ttg 336  
Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu  
100 105 110

gcc ata tcc gtc atg aac cac tgg ccc ggc gtg aaa ctg cgc gtc act 384  
Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr  
115 120 125

gaa ggc tgg gat gag gat ggt cac cat tta gaa gaa tct ttg cac tat 432  
Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr  
130 135 140

gag gga cgg gca gtg gac atc act acc tca gac agg gat aaa agc aag	480
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys	
145 150 155 160	
tat ggg atg cta tcc agg ctt gca gtg gag gca gga ttc gac tgg gtc	528
Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
165 170 175	
tat tat gaa tct aaa gcc cac ata cac tgc tct gtc aaa gca gaa aat	576
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
180 185 190	
tca gtg gct gct aaa tca gga gga tgt ttt cct ggg tct ggg acg gtg	624
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val	
195 200 205	
aca ctt ggt gat ggg acg agg aaa ccc atc aaa gat ctt aaa gtg ggc	672
Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly	
210 215 220	
gac cgg gtt ttg gct gca gac gag aag gga aat gtc tta ata agc gac	720
Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp	
225 230 235 240	
ttt att atg ttt ata gac cac gat ccg aca acg aga agg caa ttc atc	768
Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile	
245 250 255	
gtc atc gag acg tca gaa cct ttc acc aag ctc acc ctc act gcc gcg	816
Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala	
260 265 270	
cac cta gtt ttc gtt gga aac tct tca gca gct tcg ggt ata aca gca	864
His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala	
275 280 285	
aca ttt gcc agc aac gtg aag cct gga gat aca gtt tta gtg tgg gaa	912
Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu	
290 295 300	
gac aca tgc gag agc ctc aag agc gtt aca gtg aaa agg att tac act	960
Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr	
305 310 315 320	
gag gag cac gag ggc tct ttt gcg cca gtc acc gcg cac gga acc ata	1008
Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile	
325 330 335	
ata gtg gat cag gtg ttg gca tcg tgc tac gcg gtc att gag aac cac	1056
Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His	
340 345 350	
aaa tgg gca cat tgg gct ttt gcg ccg gtc agg ttg tgt cac aag ctg	1104
Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu	
355 360 365	

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn  
180 185 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val  
 195 200 205  
 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly  
 210 215 220  
 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp  
 225 230 235 240  
 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr  
 245 250 255  
 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala  
 260 265 270  
 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly  
 275 280 285  
 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln  
 290 295 300  
 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser  
 305 310 315 320  
 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro  
 325 330 335  
 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys  
 340 345 350  
 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro  
 355 360 365  
 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala  
 370 375 380  
 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg  
 385 390 395 400  
 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His  
 405 410 415  
 Pro Leu Gly Met Val Ala Pro Ala Ser  
 420 425

<210> 11  
 <211> 396  
 <212> PRT  
 <213> Murine sp.

<400> 11  
 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu  
 1 5 10 15  
 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg  
 20 25 30

Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe  
 35 40 45  
 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu  
 50 55 60  
 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn  
 65 70 75 80  
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp  
 85 90 95  
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile  
 100 105 110  
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly  
 115 120 125  
 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly  
 130 135 140  
 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly  
 145 150 155 160  
 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr  
 165 170 175  
 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu  
 180 185 190  
 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu  
 195 200 205  
 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp  
 210 215 220  
 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu  
 225 230 235 240  
 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val  
 245 250 255  
 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu  
 260 265 270  
 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro  
 275 280 285  
 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly  
 290 295 300  
 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu  
 305 310 315 320  
 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val  
 325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp  
 340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala  
 355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser  
 370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly  
 385 390 395

<210> 12  
 <211> 411  
 <212> PRT  
 <213> Murine sp.

<400> 12  
 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu  
 1 5 10 15

Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg  
 20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala  
 35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser  
 50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu  
 65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn  
 85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn  
 100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg  
 115 120 125

Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu  
 130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg  
 145 150 155 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp  
 165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser  
 180 185 190

Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala  
 195 200 205

Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys  
 210 215 220  
 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe  
 225 230 235 240  
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala  
 245 250 255  
 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr  
 260 265 270  
 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala  
 275 280 285  
 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val  
 290 295 300  
 Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val  
 305 310 315 320  
 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly  
 325 330 335  
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala  
 340 345 350  
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro  
 355 360 365  
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr  
 370 375 380  
 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr  
 385 390 395 400  
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser  
 405 410

<210> 13  
 <211> 437  
 <212> PRT  
 <213> Murine sp.

<400> 13  
 Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser  
 1 5 10 15  
 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly  
 20 25 30  
 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe  
 35 40 45  
 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu  
 50 55 60



Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	
65					70					75					80	
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	
				85					90					95		
Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	
			100					105					110			
Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
		115					120					125				
Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	
	130					135					140					
Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	
145					150					155					160	
Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
			165						170					175		
Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	
			180					185					190			
Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	
		195					200					205				
Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg	
	210					215					220					
Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	
225					230					235					240	
Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	
			245						250					255		
Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	
		260						265					270			
Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser	
		275					280					285				
Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	
	290					295					300					
Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	
305					310					315					320	
Val	Thr	Leu	Arg	Glu	Glu	Glu	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	
			325					330					335			
His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	
			340					345					350			
Ile	Glu	Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	
	355						360					365				

Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly  
 370 375 380

Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly  
 385 390 395 400

Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His  
 405 410 415

Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met  
 420 425 430

Ala Val Lys Ser Ser  
 435

<210> 14

<211> 418

<212> PRT

<213> Brachydanio rerio

<400> 14

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser  
 1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg  
 20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile  
 35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly  
 50 55 60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr  
 65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg  
 85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser  
 100 105 110

Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp  
 115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg  
 130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr  
 145 150 155 160

Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu  
 165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala  
 180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln  
 195 200 205

Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val  
 210 215 220

Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met  
 225 230 235 240

Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu  
 245 250 255

Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu  
 260 265 270

Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala  
 275 280 285

Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp  
 290 295 300

Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu  
 305 310 315 320

Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val  
 325 330 335

Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu  
 340 345 350

Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser  
 355 360 365

Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn  
 370 375 380

Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr  
 385 390 395 400

Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn  
 405 410 415

Ser Ser

<210> 15

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<223> Xaa at position 463 is any or unknown amino acid

<400> 15

Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu  
 1 5 10 15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys  
                   20                                  25                                  30  
 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile  
                   35                                  40                                  45  
 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly  
                   50                                  55                                  60  
 Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr  
                   65                                  70                                  75                                  80  
 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg  
                                   85                                  90                                  95  
 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser  
                                   100                                  105                                  110  
 Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp  
                   115                                  120                                  125  
 Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg  
                   130                                  135                                  140  
 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met  
                   145                                  150                                  155                                  160  
 Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu  
                                   165                                  170                                  175  
 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala  
                                   180                                  185                                  190  
 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu  
                   195                                  200                                  205  
 Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val  
                   210                                  215                                  220  
 Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr  
                   225                                  230                                  235                                  240  
 Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu  
                                   245                                  250                                  255  
 Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu  
                   260                                  265                                  270  
 Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser  
                   275                                  280                                  285  
 Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu  
                   290                                  295                                  300  
 Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu  
                   305                                  310                                  315                                  320

Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr  
 325 330 335  
 Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly  
 340 345 350  
 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu  
 355 360 365  
 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His  
 370 375 380  
 Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp  
 385 390 395 400  
 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr  
 405 410 415  
 Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile  
 420 425 430  
 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp  
 435 440 445  
 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser  
 450 455 460  
 Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala  
 465 470 475

<210> 16  
 <211> 411  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu  
 1 5 10 15  
 Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg  
 20 25 30  
 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala  
 35 40 45  
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser  
 50 55 60  
 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu  
 65 70 75 80  
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn  
 85 90 95  
 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn  
 100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg  
 115 120 125  
 Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu  
 130 135 140  
 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg  
 145 150 155 160  
 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp  
 165 170 175  
 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser  
 180 185 190  
 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala  
 195 200 205  
 Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg  
 210 215 220  
 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe  
 225 230 235 240  
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala  
 245 250 255  
 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr  
 260 265 270  
 Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala  
 275 280 285  
 Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val  
 290 295 300  
 Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val  
 305 310 315 320  
 Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly  
 325 330 335  
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala  
 340 345 350  
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His  
 355 360 365  
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr  
 370 375 380  
 Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser  
 385 390 395 400  
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser  
 405 410

<210> 17  
 <211> 396  
 <212> PRT  
 <213> Homo sapiens

<400> 17

Met	Ala	Leu	Leu	Thr	Asn	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu
1				5					10					15	
Ala	Leu	Pro	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
			20					25					30		
Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
		35					40					45			
Val	Pro	Gly	Val	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
	50					55					60				
Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
65					70					75					80
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
				85					90					95	
Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile
			100					105					110		
Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
		115					120					125			
Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
	130					135					140				
Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
145					150					155					160
Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
				165					170					175	
Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
			180					185					190		
Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
		195					200					205			
Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
	210					215					220				
Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
225					230					235					240
Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
				245					250					255	
Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
			260					265					270		

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro  
275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly  
290 295 300

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu  
305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val  
325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp  
340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala  
355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser  
370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly  
385 390 395

<210> 18

<211> 416

<212> PRT

<213> Brachydanio rerio

<400> 18

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile  
1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly  
20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys  
35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys  
50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile  
65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn  
85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu  
100 105 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr  
115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr  
130 135 140



Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys  
 145 150 155 160  
 Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val  
 165 170 175  
 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn  
 180 185 190  
 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val  
 195 200 205  
 Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly  
 210 215 220  
 Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp  
 225 230 235 240  
 Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile  
 245 250 255  
 Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala  
 260 265 270  
 His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala  
 275 280 285  
 Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu  
 290 295 300  
 Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr  
 305 310 315 320  
 Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile  
 325 330 335  
 Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His  
 340 345 350  
 Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu  
 355 360 365  
 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu  
 370 375 380  
 Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp  
 385 390 395 400  
 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser  
 405 410 415

&lt;210&gt; 19

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Drosophila sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1413)

&lt;400&gt; 19

atg gat aac cac agc tca gtg cct tgg gcc agt gcc gcc agt gtc acc	48
Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr	
1 5 10 15	
tgt ctc tcc ctg gga tgc caa atg cca cag ttc cag ttc cag ttc cag	96
Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln	
20 25 30	
ctc caa atc cgc agc gag ctc cat ctc cgc aag ccc gca aga aga acg	144
Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr	
35 40 45	
caa acg atg cgc cac att gcg cat acg cag cgt tgc ctc agc agg ctg	192
Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu	
50 55 60	
acc tct ctg gtg gcc ctg ctg ctg atc gtc ttg ccg atg gtc ttt agc	240
Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser	
65 70 75 80	
ccg gct cac agc tgc ggt cct ggc cga gga ttg ggt cgt cat agg gcg	288
Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala	
85 90 95	
cgc aac ctg tat ccg ctg gtc ctc aag cag aca att ccc aat cta tcc	336
Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser	
100 105 110	
gag tac acg aac agc gcc tcc gga cct ctg gag ggt gtg atc cgt cgg	384
Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg	
115 120 125	
gat tcg ccc aaa ttc aag gac ctc gtg ccc aac tac aac agg gac atc	432
Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile	
130 135 140	
ctt ttc cgt gac gag gaa ggc acc gga gcg gat ggc ttg atg agc aag	480
Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys	
145 150 155 160	
cgc tgc aag gag aag cta aac gtg ctg gcc tac tcg gtg atg aac gaa	528
Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu	
165 170 175	
tgg ccc ggc atc cgg ctg ctg gtc acc gag agc tgg gac gag gac tac	576
Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr	
180 185 190	
cat cac ggc cag gag tcg ctc cac tac gag ggc cga gcg gtg acc att	624
His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile	
195 200 205	

gcc acc tcc gat cgc gac cag tcc aaa tac ggc atg ctc gct cgc ctg	672
Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu	
210 215 220	
gcc gtc gag gct gga ttc gat tgg gtc tcc tac gtc agc agg cgc cac	720
Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His	
225 230 235 240	
atc tac tgc tcc gtc aag tca gat tgc tgc atc agt tcc cac gtg cac	768
Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His	
245 250 255	
ggc tgc ttc acg ccg gag agc aca gcg ctg ctg gag agt gga gtc cgg	816
Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg	
260 265 270	
aag ccg ctc ggc gag ctc tct atc gga gat cgt gtt ttg agc atg acc	864
Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr	
275 280 285	
gcc aac gga cag gcc gtc tac agc gaa gtg atc ctc ttc atg gac cgc	912
Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg	
290 295 300	
aac ctc gag cag atg caa aac ttt gtg cag ctg cac acg gac ggt gga	960
Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly	
305 310 315 320	
gca gtg ctc acg gtg acg ccg gct cac ctg gtt agc gtt tgg cag ccg	1008
Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro	
325 330 335	
gag agc cag aag ctc acg ttt gtg ttt gcg cat cgc atc gag gag aag	1056
Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys	
340 345 350	
aac cag gtg ctc gta cgg gat gtg gag acg ggc gag ctg agg ccc cag	1104
Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln	
355 360 365	
cga gtg gtc aag ttg ggc agt gtg cgc agt aag ggc gtg gtc gcg ccg	1152
Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro	
370 375 380	
ctg acc cgc gag ggc acc att gtg gtc aac tgc gtg gcc gcc agt tgc	1200
Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys	
385 390 395 400	
tat gcg gtg atc aac agt cag tgc ctg gcc cac tgg gga ctg gct ccc	1248
Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro	
405 410 415	
atg cgc ctg ctg tcc acg ctg gag gcg tgg ctg ccc gcc aag gag cag	1296
Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln	
420 425 430	

ttg cac agt tcg ccg aag gtg gtg agc tcg gcg cag cag cag aat ggc 1344  
Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly  
435 440 445

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atc cat tgg tat gcc aat gcg ctc tac aag gtc aag gac tac gtg ctg    1392
Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
      450                455                460

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ccg cag agc tgg cgc cac gat tga 1416  
Pro Gln Ser Trp Arg His Asp  
465 470

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<210> 20
<211> 471
<212> PRT
<213> Drosophila sp.
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<400> 20
Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
  1                      5              10              15
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Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln  
20 25 30

Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr  
35 40 45

Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu  
50 55 60

Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser  
65 70 75 80

Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala  
85 90 95

Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser  
100 105 110

Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg  
115 120 125

Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile  
130 135 140

Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys  
145 150 155 160

Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu  
165 170 175

Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr  
180 185 190

His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile  
195 200 205

Ala	Thr	Ser	Asp	Arg	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu
210						215					220				
Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Ser	Tyr	Val	Ser	Arg	Arg	His
225					230					235					240
Ile	Tyr	Cys	Ser	Val	Lys	Ser	Asp	Ser	Ser	Ile	Ser	Ser	His	Val	His
				245					250					255	
Gly	Cys	Phe	Thr	Pro	Glu	Ser	Thr	Ala	Leu	Leu	Glu	Ser	Gly	Val	Arg
			260					265					270		
Lys	Pro	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Asp	Arg	Val	Leu	Ser	Met	Thr
		275					280					285			
Ala	Asn	Gly	Gln	Ala	Val	Tyr	Ser	Glu	Val	Ile	Leu	Phe	Met	Asp	Arg
	290					295					300				
Asn	Leu	Glu	Gln	Met	Gln	Asn	Phe	Val	Gln	Leu	His	Thr	Asp	Gly	Gly
305					310					315					320
Ala	Val	Leu	Thr	Val	Thr	Pro	Ala	His	Leu	Val	Ser	Val	Trp	Gln	Pro
				325					330					335	
Glu	Ser	Gln	Lys	Leu	Thr	Phe	Val	Phe	Ala	His	Arg	Ile	Glu	Glu	Lys
			340					345					350		
Asn	Gln	Val	Leu	Val	Arg	Asp	Val	Glu	Thr	Gly	Glu	Leu	Arg	Pro	Gln
		355					360					365			
Arg	Val	Val	Lys	Leu	Gly	Ser	Val	Arg	Ser	Lys	Gly	Val	Val	Ala	Pro
	370					375					380				
Leu	Thr	Arg	Glu	Gly	Thr	Ile	Val	Val	Asn	Ser	Val	Ala	Ala	Ser	Cys
385					390					395					400
Tyr	Ala	Val	Ile	Asn	Ser	Gln	Ser	Leu	Ala	His	Trp	Gly	Leu	Ala	Pro
				405					410					415	
Met	Arg	Leu	Leu	Ser	Thr	Leu	Glu	Ala	Trp	Leu	Pro	Ala	Lys	Glu	Gln
		420						425					430		
Leu	His	Ser	Ser	Pro	Lys	Val	Val	Ser	Ser	Ala	Gln	Gln	Gln	Asn	Gly
		435					440					445			
Ile	His	Trp	Tyr	Ala	Asn	Ala	Leu	Tyr	Lys	Val	Lys	Asp	Tyr	Val	Leu
	450					455					460				
Pro	Gln	Ser	Trp	Arg	His	Asp									
465					470										

&lt;210&gt; 21

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: degenerate polypeptide sequence

<220>

<221> MOD\_RES

<222> (7)

<223> Gly, Ala, Val, Leu, Ile, Phe, Tyr or Trp

<220>

<221> MOD\_RES

<222> (9)

<223> Arg, His or Lys

<220>

<221> MOD\_RES

<222> (44)

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD\_RES

<222> (85)

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD\_RES

<222> (93)

<223> Lys, Arg, His, Asn or Gln

<220>

<221> MOD\_RES

<222> (98)

<223> Lys, Arg or His

<220>

<221> MOD\_RES

<222> (112)

<223> Ser, Thr, Tyr, Trp or Phe

<220>

<221> MOD\_RES

<222> (132)

<223> Lys, Arg or His

<220>

<221> MOD\_RES

<222> (137)

<223> Met, Cys, Ser or Thr

<220>

<221> MOD\_RES

<222> (139)

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD\_RES

<222> (181)

<223> Leu, Val, Met, Thr or Ser

<220>  
<221> MOD\_RES  
<222> (183)  
<223> His, Phe, Tyr, Ser, Thr, Met or Cys

<220>  
<221> MOD\_RES  
<222> (185)  
<223> Gln, Asn, Glu, or Asp

<220>  
<221> MOD\_RES  
<222> (186)  
<223> His, Phe, Tyr, Thr, Gln, Asn, Glu or Asp

<220>  
<221> MOD-RES  
<222> (189)  
<223> Gln, Asn, Glu, Asp, Thr, Ser, Met or Cys

<220>  
<221> MOD\_RES  
<222> (191)  
<223> Ala, Gly, Cys, Leu, Val or Met

<220>  
<221> MOD\_RES  
<222> (196)  
<223> Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser, Thr or Cys

<220>  
<221> MOD\_RES  
<222> (200)  
<223> Arg, Lys, Met or Ile

<220>  
<221> MOD\_RES  
<222> (206)  
<223> Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr or Met

<220>  
<221> MOD\_RES  
<222> (207)  
<223> Ala, Gly, Cys, Asp, Asn, Glu or Gln

<220>  
<221> MOD\_RES  
<222> (209)  
<223> Arg, Lys, Met, Ile, Asn, Asp, Glu or Gln

<220>  
<221> MOD\_RES  
<222> (211)  
<223> Leu, Val, Met or Ile

<220>  
<221> MOD\_RES  
<222> (212)

<223> Phe, Tyr, Thr, His or Trp

<220>

<221> MOD\_RES

<222> (216)

<223> Ile, Val, Leu or Met

<220>

<221> MOD\_RES

<222> (217)

<223> Met, Cys, Ile, Leu, Val, Thr or Ser

<220>

<221> MOD\_RES

<222> (219)

<223> Leu, Val, Met, Thr or Ser

<220>

<223> each Xaa may also be any amino acid.

<400> 21

Cys	Gly	Pro	Gly	Arg	Gly	Xaa	Gly	Xaa	Arg	Arg	His	Pro	Lys	Lys	Leu
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Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr
			20					25					30		
Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Xaa	Arg	Asn	Ser	Glu
		35					40					45			
Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys
	50					55					60				
Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys
65					70					75					80
Asp	Lys	Leu	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp	Pro	Gly
			85						90					95	
Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Xaa
			100					105					110		
Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser
		115					120					125			
Asp	Arg	Asp	Xaa	Ser	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala	Val	Glu
	130						135				140				
Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys
145					150					155					160
Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe
				165					170					175	
Pro	Gly	Ser	Ala	Xaa	Val	Xaa	Leu	Xaa	Xaa	Gly	Gly	Xaa	Lys	Xaa	Val
			180					185					190		



Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly  
 195 200 205

Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg  
 210 215 220

<210> 22

<211> 167

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate  
 polypeptide sequence

<220>

<221> MOD\_RES

<222> (7)

<223> Gly, Ala, Val, Leu, Ile, Pro, Phe or Tyr

<220>

<221> MOD\_RES

<222> (8)

<223> Gly, Ala, Val, Leu or Ile

<220>

<221> MOD\_RES

<222> (9)

<223> Gly, Ala, Val, Leu, Ile, Lys, His or Arg

<220>

<221> MOD\_RES

<222> (12)

<223> Lys, Arg or His

<220>

<221> MOD\_RES

<222> (13)

<223> Phe, Trp, Tyr or an amino acid gap

<220>

<221> MOD\_RES

<222> (14)

<223> Gly, Ala, Val, Leu, Ile or an amino acid gap

<220>

<221> MOD\_RES

<222> (17)

<223> Asn, Gln, His, Arg or Lys

<220>

<221> MOD\_RES

<222> (19)

<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD\_RES

<222> (22)  
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>  
<221> MOD\_RES  
<222> (27)  
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>  
<221> MOD\_RES  
<222> (29)  
<223> Ser, Thr, Gln or Asn

<220>  
<221> MOD\_RES  
<222> (30)  
<223> Met, Cys, Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>  
<221> MOD\_RES  
<222> (31)  
<223> Gly, Ala, Val, Leu, Ile or Pro

<220>  
<221> MOD\_RES  
<222> (33)  
<223> Arg, His or Lys

<220>  
<221> MOD\_RES  
<222> (40)  
<223> Gly, Ala, Val, Leu, Ile, Pro, Arg, His or Lys

<220>  
<221> MOD\_RES  
<222> (41)  
<223> Gly, Ala, Val, Leu, Ile, Phe or Tyr

<220>  
<221> MOD\_RES  
<222> (44)  
<223> Arg, His or Lys

<220>  
<221> MOD\_RES  
<222> (45)  
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>  
<221> MOD\_RES  
<222> (46)  
<223> Thr or Ser

<220>  
<221> MOD\_RES  
<222> (48)  
<223> Gly, Ala, Val, Leu, Ile, Asn or Gln

<220>  
<221> MOD\_RES  
<222> (53)  
<223> Arg, His or Lys

<220>  
<221> MOD\_RES  
<222> (54)  
<223> Asp or Glu

<220>  
<221> MOD\_RES  
<222> (71)  
<223> Ser or Thr

<220>  
<221> MOD\_RES  
<222> (79)  
<223> Glu, Asp, Gln or Asn

<220>  
<221> MOD\_RES  
<222> (83)  
<223> Glu or Asp

<220>  
<221> MOD\_RES  
<222> (84)  
<223> Arg, His or Lys

<220>  
<221> MOD\_RES  
<222> (85)  
<223> Gly, Ala, Val, Leu or Ile

<220>  
<221> MOD\_RES  
<222> (87)  
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>  
<221> MOD\_RES  
<222> (95)  
<223> Met, Cys, Gln, Asn, Arg, Lys or His

<220>  
<221> MOD\_RES  
<222> (100)  
<223> Arg, His or Lys

<220>  
<221> MOD\_RES  
<222> (107)  
<223> Trp, Phe, Tyr, Arg, His or Lys

<220>  
<221> MOD\_RES  
<222> (114)

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr or Phe

<220>

<221> MOD\_RES

<222> (115)

<223> Gln, Asn, Asp or Glu

<220>

<221> MOD\_RES

<222> (116)

<223> Asp or Glu

<220>

<221> MOD\_RES

<222> (125)

<223> Gly, Ala, Val, Leu, or Ile

<220>

<221> MOD\_RES

<222> (134)

<223> Arg, His or Lys

<220>

<221> MOD\_RES

<222> (135)

<223> Asn, Gln, Thr or Ser

<220>

<221> MOD\_RES

<222> (139)

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Met or Cys

<220>

<221> MOD\_RES

<222> (141)

<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>

<221> MOD\_RES

<222> (157)

<223> Arg, His or Lys

<220>

<221> MOD\_RES

<222> (158)

<223> Asn, Gln, Gly, Ala, Val, Leu or Ile

<220>

<221> MOD\_RES

<222> (160)

<223> Gly, Ala, Val, Leu or Ile

<220>

<221> MOD\_RES

<222> (162)

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr or Cys

<220>

<221> MOD\_RES  
 <222> (166)  
 <223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>  
 <221> MOD\_RES  
 <222> (167)  
 <223> Asp or Glu

<220>  
 <223> each Xaa may also be any amino acid.

<400> 22  
 Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys  
   1                  5                  10                  15  
 Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu  
                   20                  25                  30  
 Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa  
           35                  40                  45  
 Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile  
   50                  55                  60  
 Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg  
   65                  70                  75                  80  
 Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp  
                   85                  90                  95  
 Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His  
           100                  105                  110  
 His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr  
   115                  120                  125  
 Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala  
   130                  135                  140  
 Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa  
 145                  150                  155                  160  
 His Xaa Ser Val Lys Xaa Xaa  
                   165

<210> 23  
 <211> 627  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(624)

&lt;400&gt; 23

atg tgg aaa tgg ata ctg aca cat tgt gcc tca gcc ttt ccc cac ctg	48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	
1 5 10 15	
ccc ggc tgc tgc tgc tgc tgc tgc ttt ttg ttg ctg ttc ttg gtg tct tcc	96
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	
20 25 30	
gtc cct gtc acc tgc caa gcc ctt ggt cag gac atg gtg tca cca gag	144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	
35 40 45	
gcc acc aac tct tct tcc tcc tcc ttc tcc tct cct tcc agc gcg gga	192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly	
50 55 60	
agg cat gtg cgg agc tac aat cac ctt caa gga gat gtc cgc tgg aga	240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	
65 70 75 80	
aag cta ttc tct ttc acc aag tac ttt ctc aag att gag aag aac ggg	288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	
85 90 95	
aag gtc agc ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag	336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	
100 105 110	
ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc	384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	
115 120 125	
aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa	432
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	
130 135 140	
gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga	480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly	
145 150 155 160	
tac aat acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg	528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met	
165 170 175	
tat gtg gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca	576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr	
180 185 190	
cga agg aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca	624
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
195 200 205	
tag	627

&lt;210&gt; 24

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

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Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
 1           5           10           15

Pro Gly Cys Cys Cys Cys Phe Leu Leu Phe Leu Val Ser Ser
      20           25           30

Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
      35           40           45

Ala Thr Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
      50           55           60

Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
      65           70           75           80

Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
      85           90           95

Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
      100          105          110

Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
      115          120          125

Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
      130          135          140

Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
      145          150          155          160

Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
      165          170          175

Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
      180          185          190

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
      195          200          205

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&lt;210&gt; 25

&lt;211&gt; 74

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 25

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gcgcgcttcg aagcgaggca gccagcgagg gagagagcga gcgggagcgc cggagcgagg 60
aaatcgatgc gcgc

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<210> 26  
 <211> 74  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 26  
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 cgggatccgc gcgc 74

<210> 27  
 <211> 996  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: gene  
 activation construct

<400> 27  
 cgaagcgagg cagccagcga gggagagagc gagcgggcca gccggagcga ggaaatcgaa 60  
 ggttcgaatc cttccccac caccatcact ttcaaaagtc cgaaagaatc tgctccctgc 120  
 ttgtgtgttg gaggtcgctg agtagtgccg gagtaaaatt taagctacaa caaggcaagg 180  
 cttgaccgac aattgcatga agaactctgct taggggttagg cgttttgccc tgcttcgcga 240  
 tgtacggggc agatatacgc gttgacattg attattgact agttattaat agtaatcaat 300  
 tacgggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 360  
 tggcccgctt ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 420  
 tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggact atttacggta 480  
 aactgcccac ttggcagtac atcaagtgtg tcatatgccg agtacgcccc ctattgacgt 540  
 caatgacggg aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 600  
 tacttggcag tacatctacg tattagtcac cgctattacc atgggtgatgc ggttttggca 660  
 gtacatcaat gggcgtggat agcggtttga ctcacgggga tttccaagtc tccaccccat 720  
 tgacgtcaat gggagtttgt tttggcacca aaatcaacgg gactttccaa aatgtcgtaa 780  
 caactccgcc ccattgacgc aaatgggcgg taggcgtgta cgggtggagg tctatataag 840  
 cagagctctc tggctaacta gagaaccac tgcttactgg cttatcgaaa ttaatacgac 900  
 tcactatagg gagaccaag cttggtaccg agctcggatc gatctgggaa agcgcaagag 960  
 agagcgaca cgcacacacc cgccgcgcgc actcgg 996



<210> 28  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: antisense  
construct

<400> 28  
gtcctggcgc cgccgccgcc gtcgcc 26

<210> 29  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: antisense  
construct

<400> 29  
ttccgatgac cggcctttcg cggtga 26

B!  
Cmt  
<210> 30  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: antisense  
construct

<400> 30  
gtgcacggaa aggtgcaggc cacact 26